

1/10

ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA	50
M A L E Q N Q S T D Y Y Y E E N E	
AATGAATGGC ACTTATGACT ACAGTCAATA TGAAGTATC TGTATCAAAG	100
M N G T Y D Y S Q Y E L I C I K E	
AAGATGTCAG AGAATTTGCA AAAGTTTTC TCCCTGTATT CCTCACAATA	150
D V R E F A K V F L P V F L T I	
GTTTTCGTCA TTGGACTTGC AGGCAATTCC ATGGTAGTGG CAATTTATGC	200
V F V I G L A G N S M V V A I Y A	
CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG	250
Y Y K K Q R T K T D V Y I L N L A	
CTGTAGCAGA TTTACTCCTT CTATTCATC TGCCTTTTTG GGCTGTTAAT	300
V A D L L L L L F T L P F W A V N	
GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC	350
A V H G W V L G K I M C K I T S A	
CTTGACACA CTAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA	400
L Y T L N F V S G M Q F L A C I S	
GCATAGACAG ATATGTGGCA GTAACATAAG TCCCCAGCCA ATCAGGAGTG	450
I D R Y V A V T K V P S Q S G V	
GGAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT	500
G K P C W I I C F C V W M A A I L	
GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC AATGCTAGGT	550
L S I P Q L V F Y T V N D N A R C	
GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT	600
I P I F P R Y L G T S M K A L I	
CAATGCTAG AGATCTGCAT TGGATTGTGA GTACCCTTTC TTATTATGGG	650
Q M L E I C I G F V V P F L I M G	
GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA	700
V C Y F I T A R T L M K M P N I K	
AAATATCTCG ACCCCTAAAA GTTCTGCTCA CAGTCGTTAT AGTTTTTATT	750
I S R P L K V L L T V V I V F I	
GTCACTCAAC TGCCTTATAA CATGTGCAAG TTCTGCCGAG CCATAGACAT	800
V T Q L P Y N I V K F C R A I D I	
CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG	850
I Y S L I T S C N M S K R M D I A	
CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA	900
I Q V T E S I A L F H S C L N P	
ATCCTTTATG TTTTATGGG AGCATCTTTC AAAAATACTAG TTATGAAAGT	950
I L Y V F M G A S F K N Y V M K V	
GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT	1000
A K K Y G S W R R Q R Q S V E E F	
TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT	1050
P F D S E G P T E P T S T F S I	
TAAAGGTAAA ACTGCTCTGC CTTTGTCTTG GATACATATG AATGATGCTT	1100
- R - N C S A F C L D T Y E - C F	
TCCCCTCAAA TAAACATCT GCCTTATTCT GAAAAAATA AAAAAAM	1147
P L K N I C L I L K K K K K	

FIG. 1

CCX-CKR MALEQNQSTDYVYE--ENEMNGTV-----DYSQYELICIK 33
 CCR9 MTPTDFTSPIPNMADDYG-SESTSSM-EDYVN----FNFTDF--YCEK
 CCR7 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLCSK
 CCR6 MSGESMNFSDVFDSSDYFVS-----VNTSYYS-----VDSEML--LCSL
 STRL33 MAEHDYHEDYGFSGS-----SF-NDSSQEEHQDF--L---

TM1

CCX-CKR EDVREFAKVFLVFLTIVFVIGIAGNSMVVAIMAYYKKQRTKTDVYILNL 83
 CCR9 NNVRQFASHFLPPLYWLVIIVGALGNSLVILVYWCYTRVKITMTDMFLNL
 CCR7 KDVRNFKAWFLPIMYSIICFVGILLGNGLVLTITTYFKRLKITMTDTYILNL
 CCR6 QEVROFSRLFVPIAYSLLICVFGILLGNILVITFAFYKKARSMTDVYILNM
 STRL33 ----QESKVFLPCMYLVVFVCGLVGNSIMLVISIFYHKLQSLTDVFLVNL

TM2

TM3

CCX-CKR AVADLLLLFTLPFWAV-NAVHGWLCKIMCKITTSALYTLNFMVSGMOFLAC 132
 CCR9 ATADLLFLVTLFPWAIA-AADQWKFOFMCKVVNSMYKMFYSCVLLIMC
 CCR7 AVADILFLLTLFPWAYS-AAKSWVFGVHFCKLIFAIVKMSFFSGMLILLC
 CCR6 ATADILFVLTLFPWAVSHATGAWVFSNATCKLLKGIYAINFNCGMLLLTC
 STRL33 PLADLVFVCTLPFWAYA-GIHEWVFGQVMCKSLLGIYTLNFEYTSMLILTC

TM4

CCX-CKR ISIDRYVAVTK-VPSQSGVGKP---CWIIICFCVWMAAILLSIFQLVFYTV 178
 CCR9 ISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIIVLAALCIHEILYSQI
 CCR7 ISIDRYVAVIQAVSAHRHARVLLISKLSVGSAILATVLSIBELLYSDL
 CCR6 ISMURYIAIVQATKSFRRLRSRTLPRTKIICLVVWGLSVIISSTFVFNQK
 STRL33 ITVDRFIVVVKATKAYNQQAQRMTWGKVTSLLIWISLLVSLPQIIYGNV

TM5

CCX-CKR NDNAR---CIPIFPRY-LGTSMKALIQMLEICIGFVVPFLIMGVCYFITA 224
 CCR9 KEESGIAICTMVYPS-DESKLKSAVLTLLKVILGFFLPFVVMACCYTII
 CCR7 QRSSEQAMRCSLIT-EHVEAF-ITIQAQMVIGFLVPLLAMSFICYLVII
 CCR6 YNTQGSVDVCEPKYQTVSEPIRWKLLMLGLLELLFGFFIPLMFMIFCYTFIV
 STRL33 FNLDKL-IC--GYH--DEAIS--TVVLATQMTLGEFLPLLTMIVCYSVII

TM6

CCX-CKR RTLKMKMFIKISRFLKVLTLVIVFIVTOLPYNIVKFCRAIDIIYSLITS 274
 CCR9 HTLIQAKKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISN
 CCR7 RTLQARNFERNKAIKVIIAVVVFIVFOLPYNIGVLAQTVANFNITSST
 CCR6 KTLVQAQNSKRHKAIKRMIIAVVLVFLACQIPHNMLLV-TAANLGKMNRS
 STRL33 KTLHAGGFQKHRSLKIIFLVMAVELLTOMPFNLMKFIRSTH-----WE

FIG. 2A

TM7

CCX-CKR	CNMSKRMDTIAIQVTESIALFHSCLNPILYVFMGASFKNYVMK-----V	317
CCR9	CAVSTNIDICFQVTQTIAFFHSCLNPILYVFGERFRDLVKTLKNLGC	
CCR7	CELSKQLNTAYDVTYSLACVRCCVNFPLYAFIGVKFRNDIFKLFKDLGCL	
CCR6	CQSEKLIGYTKTVTEVLAFLHCLNPILYAFIGQKFRNYFLKILKDLWCV	
STRL33	YYAMTSFHYTIMVTEALAYLRACLNPILYAFVSLKFRKNFWKLVKDIGCL	

CCX-CKR	AKKY--GSWRRQRQSVEEFPFDSEGP--TEPTSTFSI	350
CCR9	SQA-QWVSFTR---REGSLK-LSSMLLETTSGALSL	
CCR7	SQE-QLRQWSS---CRHIRR-SSMSVEAETTTTFSP	
CCR6	RRKYKSSGFCAGRYSENISRQTSETADNDNASSTFM	
STRL33	P--Y--LGVSHQWKSSSEDNSKTFSSASHNVEATSMFQL	

FIG. 2A
(CONTINUED)

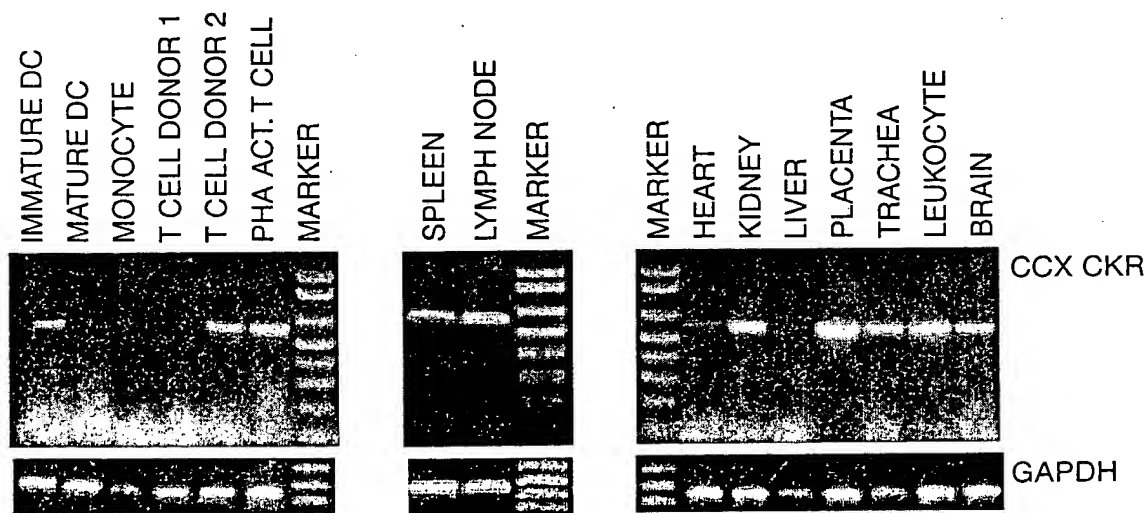


FIG. 2B

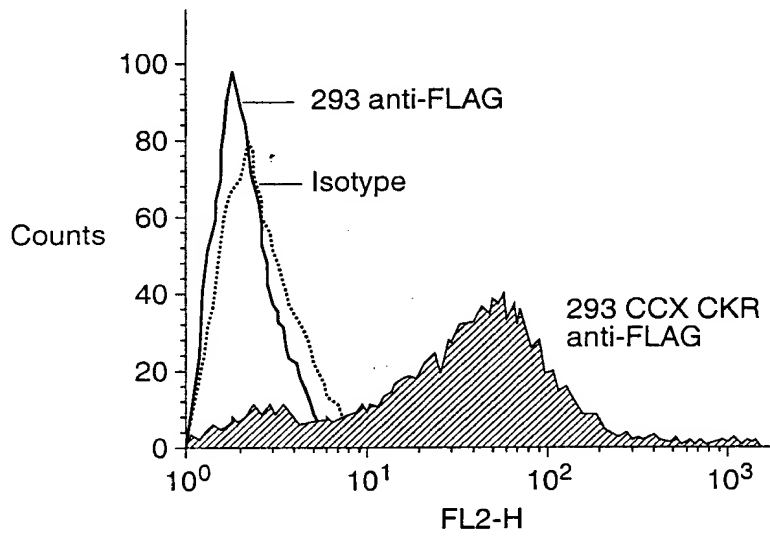


FIG. 2C

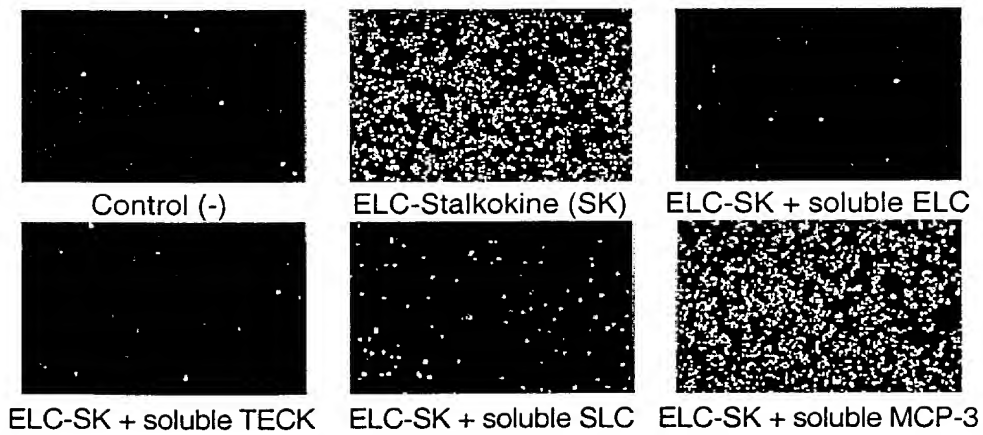


FIG. 3A

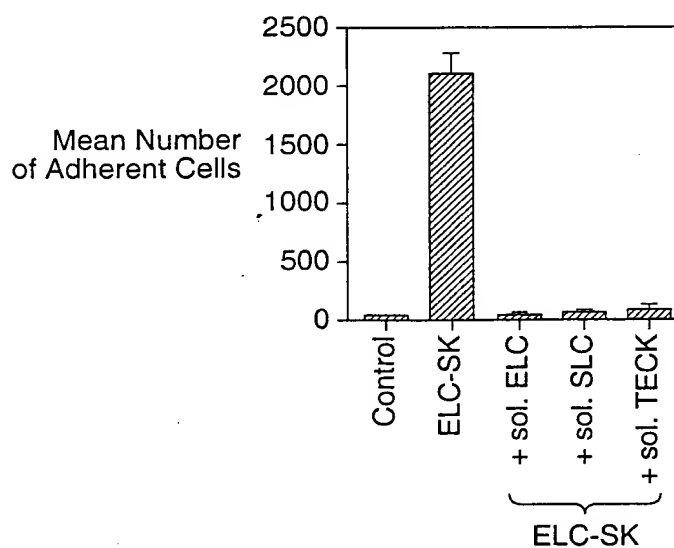


FIG. 3B

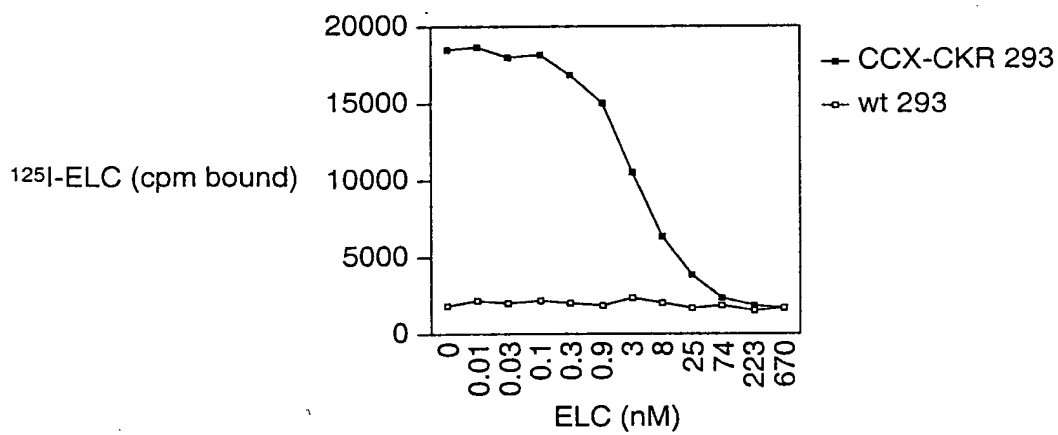


FIG. 3C

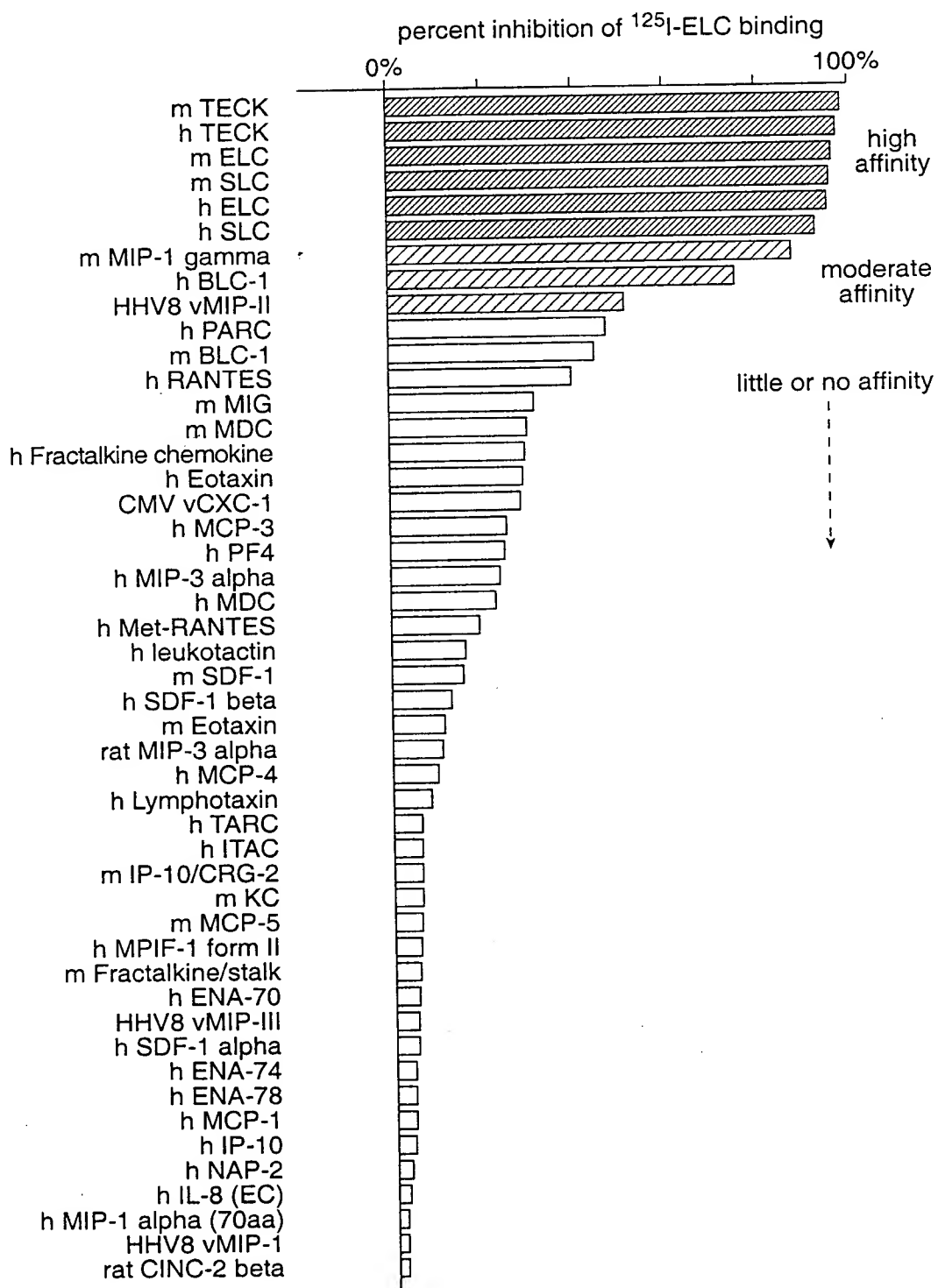


FIG. 4A

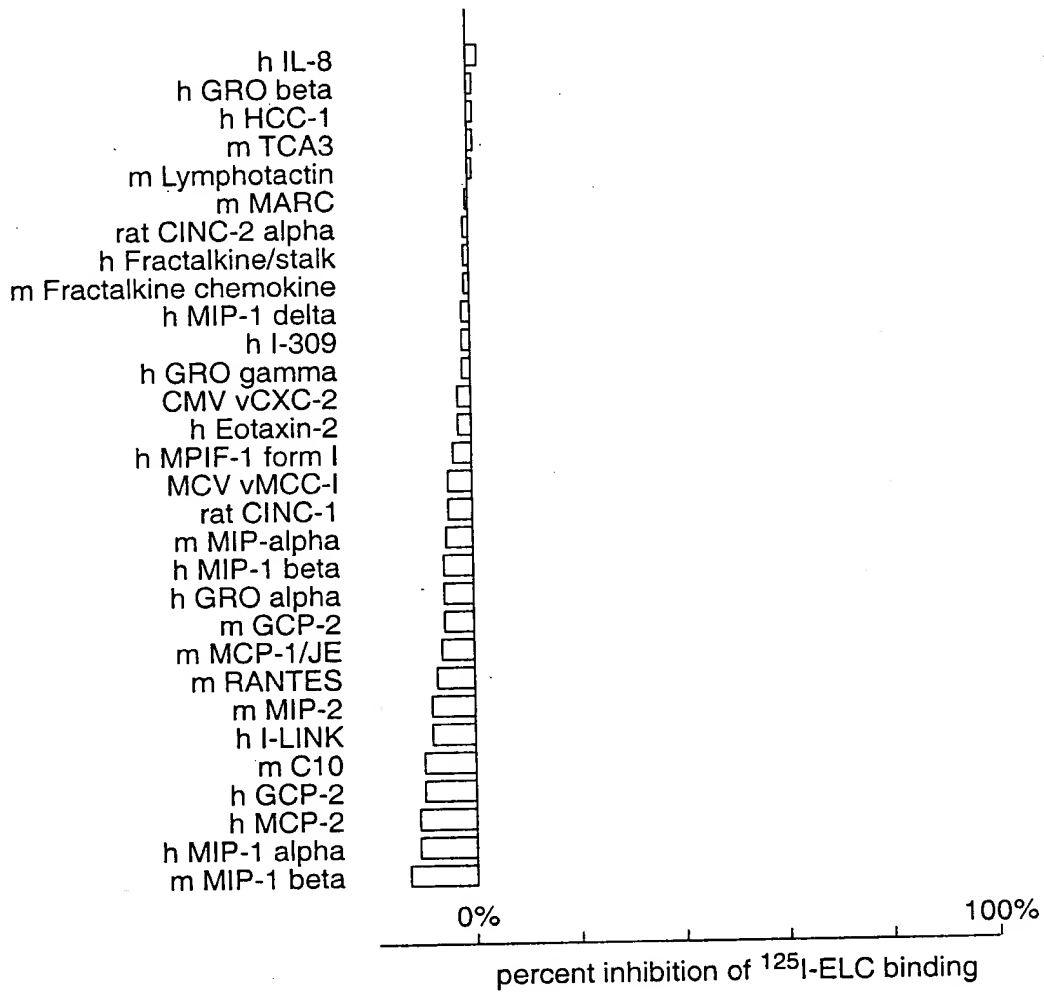
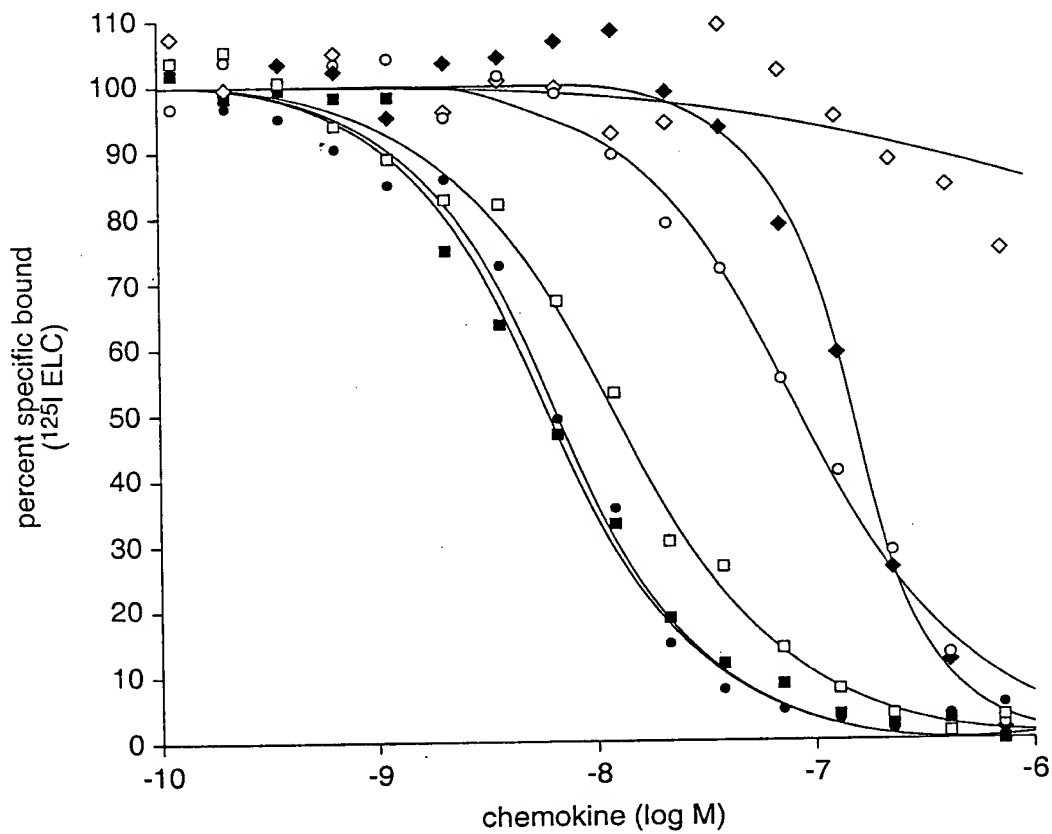


FIG. 4A
(CONTINUED)



human chemokines		murine chemokines	
	<u>IC-50</u>		<u>IC-50</u>
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

5'upstream CCXCKR	ATGCAGCATC	TCGTTTATAA	AAGGCAACTA	GTGAAATTTA	GTGCAAATGC	50
5'upstream CCXCKR	TGAGAGAATT	TATTTAACTT	ATTTAAATTA	AATTTATAAA	TAACATCAAA	100
5'upstream CCXCKR	ATAAAAAATA	AATTTAATTT	AAATAAACCA	AGTAATTTGC	TATTTTCGTT	150
5'upstream CCXCKR	TTTATTCAAT	TTGTTGTAGA	TATACTTTTA	CGATTCACAA	AATTATGTAT	200
5'upstream CCXCKR	GTAAAGATTA	TAACACTATT	TATTCTTTTT	AGTTAAAATC	TAATTAAATT	250
5'upstream CCXCKR	TTCATATTTT	AAAAATCATT	TTTACATAAA	AGTCTTCACT	TTTATTTAGG	300
5'upstream CCXCKR	ATTTAATGAT	TAAGAAAATT	CTCCAGGGCA	TTATGTTTAT	TGTCCTGTTC	350
5'upstream CCXCKR	AAATCCAAGC	TCTTTCACAC	AGAATTGTAC	AAGCAAAGTT	TGAGTAACTA	400
5'upstream CCXCKR	ATCTTGGGGT	CATATTCCAA	TGTGGCTCCC	ATTAAAGCAT	TTCAAAGAGT	450
5'upstream CCXCKR	GCTAGATTCA	GGCTCACATA	TGTTACAGCA	ACAGGCTATA	CTCTAGGGAA	500
5'upstream CCXCKR	AGAACAAAAC	AGCTTGATAG	AAACTGTGTG	CTTTTAAGCA	TATTTAGACA	550
TRANSLATION START →						
5'upstream CCXCKR	AATATCTATC	CTGTATTCTC	TTTGCCATCT	AGATTGGAGC	CATGGCTTTG ATGGCTTTG	600 9
5'upstream CCXCKR	GAACAGAACC	GTCAACAGA	TTATTATTAT	GAGGACAAGT	GAAATGAATG	649
	GAACAGAACC	AGTCAACAGA	TTATTATTAT	GAGGA- AAAT	GAAATGAATG	58
5'upstream CCXCKR	GC-CTGATGA	CTACAGTCAG	TATGAACTGA	TCTGT	TC	685
	GCACTTATGA	CTACAGTCAA	TATGAACTGA	TCTGTATCAA	AGAAGATGTC	108
5'upstream CCXCKR	AGAGAAAGAGA	CAGAGGATAT	GC-ACAGGGT	TGCTCCCTGT	ATTGCTCACC	734
	AGAGAA	-----TIT	GCAAAAGTTT	TCCTCCCTGT	ATTCCTCACA	147
5'upstream CCXCKR	ATAG	-----	-----	-----AG	-----	740
	ATAGTTTTTCG	TCATTGGACT	TGCAGGCAAT	TCCATGGTAG	TGGCAATTTA	197
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	TGCCTATTAC	AAGAAACAGA	GAACCAAAAC	AGATGTGTAC	ATCCTGAATT	247
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	TGGCTGTAGC	AGATTTACTC	CTTCTATTCA	CTCTGCCTTT	TTGGGCTGTT	297
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
	AATGCAGTTC	ATGGGTGGGT	TTTAGGGAAA	ATAATGTGCA	AAATAACTTC	347

FIG. 5

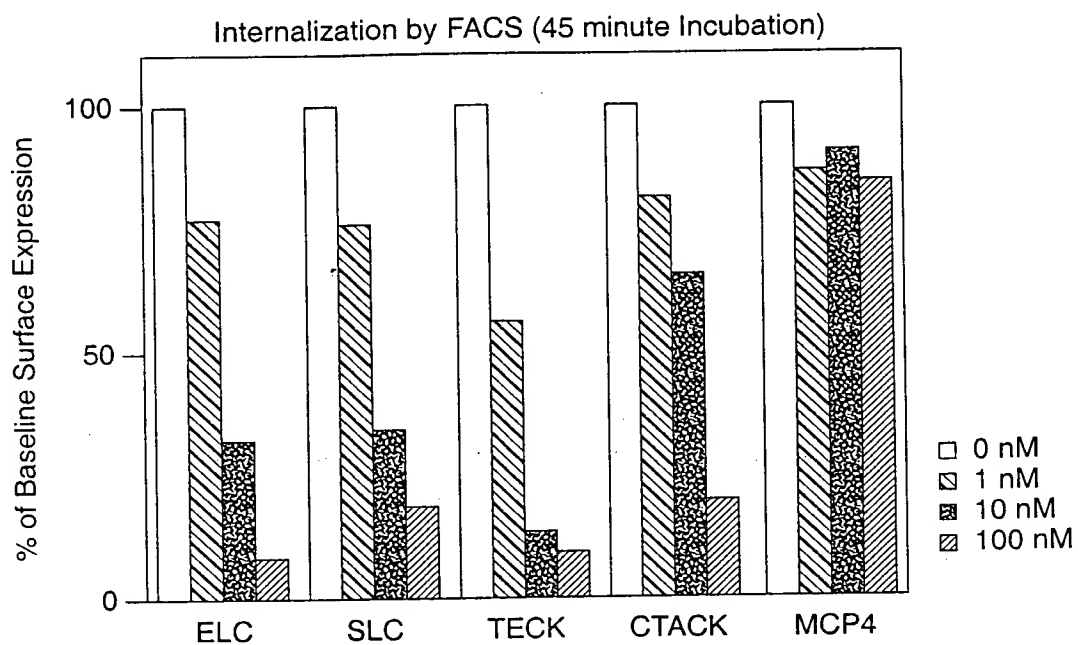


FIG. 6A

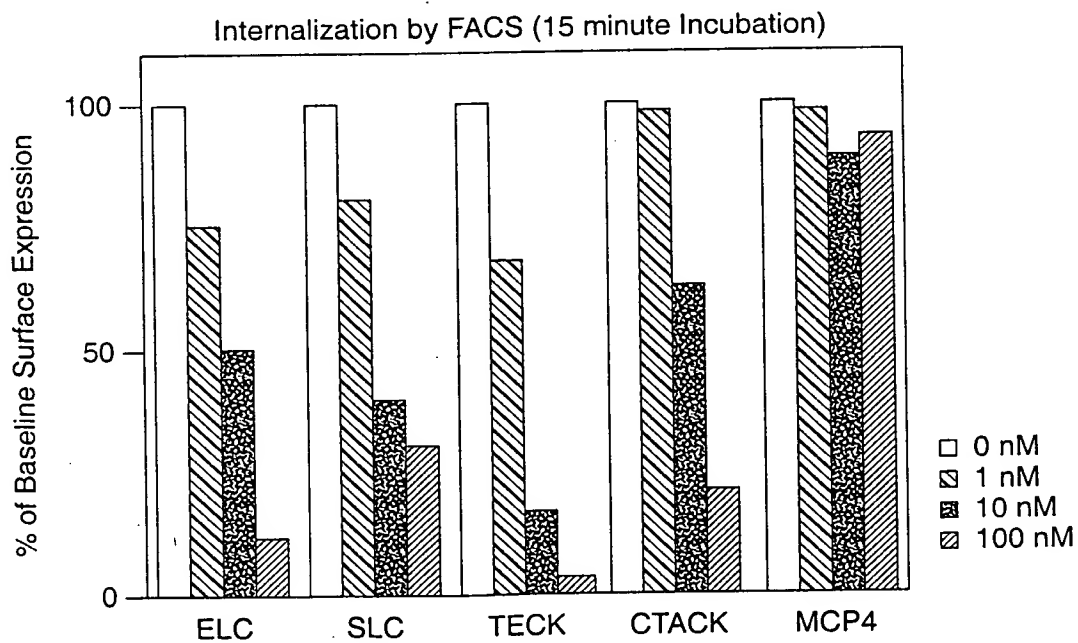


FIG. 6B